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DB 181 APPELADLRSEFEVEFKRKRWODISMMKKTIGENILAHIOHEVPLECMVDVDFUD 240
QY 244 KFEVETLGESEVAOLQAMWYKADPNDFEYERKRKESAAVLPFGEDFYHAAIPGTPQVL 292
DB 241 HFEVETLGESEVAOLQAMWYKADPNDFEYERKRKESAAVLPFGEDFYHAAIPGTPQVL 300
QY 293 NTFGEFCRGLIKKRNKDLFAAMHDESHLNKYFLINKPTKILSPRYCMYHIGLADIKLV 352
DB 401 NTFGEFCRGLIKKRNKDLFAAMHDESHLNKYFLINKPTKILSPRYCMYHIGLADIKLV 360
QY 444 KMSWGTREYNNVNNV 368
DB 461 KMSWGTREYNNVNNV 376

RESULT 2
QY0065 PRELIMINARY: PKT: 274 AA.
QY0065
AC 070065
DB 01 MAY-2000 (TREMUR: 13, Created)
DB 01 MAY-2000 (TREMUR: 13, Last sequence update)
DB 01 MAY-2000 (TREMUR: 13, Last annotation update)
DB CDS AN SPECIFIC ALPHA 1-3 N ACETYLAALACTOSAMINYLTRANSFERASE
DB (FRAGMENT).
DB ABO.
DB Homo sapiens (Human).
DB Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DB Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
DB NCBI_TaxID=9606;
DB 111
DB SEQUENCE FROM N.A.
DB Yamamoto F.;
DB "Human histo-blood group Abo gene locus alleles."
DB Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DB EMBL: AF134420; AA026576.1;
DB FEM: AF134420; AA026576.1; JOINED.
DB Translated.
DB NON_TER 1
DB 274
DB SEQUENCE 274 AA: 31991 MW: 6786627028E2955 CRC64;
SO

Query Match 43.08; Score 662; DB 4; Length 274;
Best Local Similarity 45.68; Pred. No. 1e-46;
Matches 125; Conservative 50; Mismatches 97; Indels 2; Gaps 2;

QY 94 RFEVVTMKKRAVNVWEGTYNKAVALDNYAKOKITVGLTFVAGVLEHYLEFETSANK 153
DB 1 RFEVVTMKKRAVNVWEGTYNKAVALDNYAKOKITVGLTFVAGVLEHYLEFETSANK 159
QY 154 HFEVGHVTFEYIMVDSRMLLEGLRSEFVEKLRPEKRWODISMMKKTIGENIVAH 213
DB 60 HFEVGHVTFEYIMVDSRMLLEGLRSEFVEKLRPEKRWODISMMKKTIGENIVAH 119
QY 214 LGHEVDFLECMVDVDFUDRKGVETLGESEVAOLQAMWYKADPNDFEYERKRKESAAVLPFG 273
DB 120 FLSSEVDVLCVDMEDRHHVVEILPLFGLTDPGFSSREAFTEYERKPOSQAVLPKD 179
QY 274 EGDFFYHAAIPGTPQVLNITGEFCRGLIKKRNKDLFAAMHDESHLNKYFLINKPTKIL 333
DB 180 EGDFFYHAAIPGTPQVLNITGEFCRGLIKKRNKDLFAAMHDESHLNKYFLINKPTKIL 219
QY 444 SHPEYCMYHIGLADIKLVKMSWGTREYNNV 366
DB 240 SHPEYCMYHIGLADIKLVKMSWGTREYNNV 273

RESULT 3
QY0068 PRELIMINARY: PKT: 274 AA.
AC 070068
DB 01 MAY-2000 (TREMUR: 13, Created)
DB 01 MAY-2000 (TREMUR: 13, Last sequence update)

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DB 01 MAY-2000 (TREMUR: 13, Last annotation update)
DB A1 SPECIFIC ALPHA 1-3 N ACETYLAALACTOSAMINYLTRANSFERASE (FRAGMENT).
DB ABO.
DB Homo sapiens (Human).
DB Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DB Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
DB NCBI_TaxID=9606;
DB 111
DB SEQUENCE FROM N.A.
DB Yamamoto F.;
DB "Human histo-blood group Abo gene locus alleles."
DB Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DB EMBL: AF134420; AA026576.1;
DB FEM: AF134420; AA026576.1; JOINED.
DB Translated.
DB NON_TER 1
DB 274
DB SEQUENCE 274 AA: 31977 MW: 7180470668E208A CRC64;
SO

Query Match 42.88; Score 658; DB 4; Length 274;
Best Local Similarity 45.78; Pred. No. 2.1e-46;
Matches 124; Conservative 50; Mismatches 98; Indels 2; Gaps 2;

QY 94 RFEVVTMKKRAVNVWEGTYNKAVALDNYAKOKITVGLTFVAGVLEHYLEFETSANK 153
DB 1 RFEVVTMKKRAVNVWEGTYNKAVALDNYAKOKITVGLTFVAGVLEHYLEFETSANK 159
QY 154 HFEVGHVTFEYIMVDSRMLLEGLRSEFVEKLRPEKRWODISMMKKTIGENIVAH 213
DB 60 HFEVGHVTFEYIMVDSRMLLEGLRSEFVEKLRPEKRWODISMMKKTIGENIVAH 119
QY 214 LGHEVDFLECMVDVDFUDRKGVETLGESEVAOLQAMWYKADPNDFEYERKRKESAAVLPFG 273
DB 120 FLSSEVDVLCVDMEDRHHVVEILPLFGLTDPGFSSREAFTEYERKPOSQAVLPKD 179
QY 274 EGDFFYHAAIPGTPQVLNITGEFCRGLIKKRNKDLFAAMHDESHLNKYFLINKPTKIL 333
DB 180 EGDFFYHAAIPGTPQVLNITGEFCRGLIKKRNKDLFAAMHDESHLNKYFLINKPTKIL 219
QY 334 SHPEYCMYHIGLADIKLVKMSWGTREYNNV 366
DB 240 SHPEYCMYHIGLADIKLVKMSWGTREYNNV 273

RESULT 4
QY0591 PRELIMINARY: PKT: 295 AA.
AC 015951
DB 01 NOV-1996 (TREMUR: 01, Created)
DB 01 NOV-1996 (TREMUR: 09, Last sequence update)
DB 01 NOV-1996 (TREMUR: 12, Last annotation update)
DB HISTO-BLOOD GROUP A2 TRANSFERASE (FRAGMENT).
DB ABO.
DB Homo sapiens (Human).
DB Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DB Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
DB NCBI_TaxID=9606;
DB 111
DB SEQUENCE FROM N.A.
DB MEDLINE:9249251; PubMed:1520122;
DB Yamamoto F.; McNeill P.D.; Hakomori S.;
DB "Human histo-blood group A2 transferase coded by A2 allele, one of the
DB A subtypes, is characterized by a single base deletion in the coding
DB RT sequence, which results in an additional domain at the carboxyl
DB RT terminal."
DB Biochem. Biophys. Res. Commun. 187:366-374(1992).
DB 121
DB SEQUENCE FROM N.A.
DB Yamamoto F.;
DB "Human histo-blood group Abo gene locus alleles."
DB Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DB EMBL: S44054; AA023167.1;

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DR EMBL: AF134422: AAD26577.1: -  
 DR EMBL: AF134421: AAD26577.1: JOINED.  
 KW Transferrase.  
 FT NON\_TER 1  
 SO SEQUENCE 295 AA: 34194 MW: 0DA31B71906BF5B8 CRC64:

Query Match 32.8%; Score 658; DR 4; Length 295;  
 Best Local Similarity 45.3%; Pred. No. 2.4e-46;  
 Matches 124; Conservative 50; Mismatches 98; Indels 2; Gaps 2;

QY 94 RPEVMTMKKAPVWEGTSTNRAVLDNYAKOKITVGLTFVAVGRTYEHYLEEFTLSANK 153  
 1 RKDVLVVTPLAPLAWGECTFNIDILNEQFRLONTITGLTFVAKKYVA-FLKLFLETAEK 59  
 DB 140 HFVGHVHYVFTDQAAVRAVTLTGROSLVLEVAVKMKQDVSMRBMISDFCERK 199

QY 154 HFVGHVHYFTIMVDVSRMPLIEGLRSKVKIKPEKRMODISMRRKKTIGEHIVAH 213  
 DB 214 IOHEVDLFCMDVQVQDKRGVETLGEVSAOOLAMWKADPNDFYERKRESAAYIPFG 273  
 DB 260 EGDFFYHAIIGGPTPOVNLITQECFKGLDKKNDIEAOMHDSHLNKKYFLNKPITKL 333  
 DB 320 SPEYLMDOQLGMPAVLRLKRLFTAVPKHQAVERN 353

QY 334 SPEYCMWYH-IGLPADIKLVKMSQTKKEYNVARN 366  
 DB 240 SPEYLMDOQLGMPAVLRLKRLFTAVPKHQAVERN 273

RESULT 5  
 ID 014490 PRELIMINARY: PRT: 354 AA.  
 AC Q14490:  
 DT 01-NOV-1996 (TREMBlrel. 01, created)  
 DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, last annotation update)  
 DE B(A)-SPECIFIC ALPHA 1->3 GALACTOSYLTRANSFERASE (FRAGMENT).  
 GN ABO.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RA Yamamoto F.;  
 RT "Human histo-blood group ABO gene locus alleles";  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF134422: AAD26577.1: -  
 DR EMBL: AF134421: AAD26577.1: JOINED.  
 KW Transferrase.  
 FT NON\_TER 1  
 SO SEQUENCE 295 AA: 34194 MW: 0DA31B71906BF5B8 CRC64:

QY 94 RPEVMTMKKAPVWEGTSTNRAVLDNYAKOKITVGLTFVAVGRTYEHYLEEFTLSANK 153  
 1 RKDVLVVTPLAPLAWGECTFNIDILNEQFRLONTITGLTFVAKKYVA-FLKLFLETAEK 59  
 DB 140 HFVGHVHYVFTDQAAVRAVTLTGROSLVLEVAVKMKQDVSMRBMISDFCERK 199

QY 154 HFVGHVHYFTIMVDVSRMPLIEGLRSKVKIKPEKRMODISMRRKKTIGEHIVAH 213  
 DB 214 IOHEVDLFCMDVQVQDKRGVETLGEVSAOOLAMWKADPNDFYERKRESAAYIPFG 273  
 DB 260 EGDFFYHAIIGGPTPOVNLITQECFKGLDKKNDIEAOMHDSHLNKKYFLNKPITKL 333  
 DB 320 SPEYLMDOQLGMPAVLRLKRLFTAVPKHQAVERN 353

QY 334 SPEYCMWYH-IGLPADIKLVKMSQTKKEYNVARN 366  
 DB 240 SPEYLMDOQLGMPAVLRLKRLFTAVPKHQAVERN 273

RESULT 6  
 ID 090063 PRELIMINARY: PRT: 274 AA.  
 AC 090063:  
 DT 01-MAY-2000 (TREMBlrel. 13, created)  
 DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, last annotation update)  
 DE B(A)-SPECIFIC ALPHA 1->3 GALACTOSYLTRANSFERASE (FRAGMENT).  
 GN ABO.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RA Yamamoto F.;  
 RT "Human histo-blood group ABO gene locus alleles";  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF134422: AAD26577.1: -  
 DR EMBL: AF134421: AAD26577.1: JOINED.  
 KW Transferrase; Glycosyltransferase.  
 FT NON\_TER 1  
 SO SEQUENCE 274 AA: 31894 MW: 65F322FA302HFA73 CRC64:

Query Match 32.7%; Score 656; DR 4; Length 274;  
 Best Local Similarity 45.6%; Pred. No. 3.1e-46;  
 Matches 125; Conservative 48; Mismatches 99; Indels 2; Gaps 2;

QY 94 RPEVMTMKKAPVWEGTSTNRAVLDNYAKOKITVGLTFVAVGRTYEHYLEEFTLSANK 153  
 1 RKDVLVVTPLAPLAWGECTFNIDILNEQFRLONTITGLTFVAKKYVA-FLKLFLETAEK 59  
 DB 140 HFVGHVHYVFTDQAAVRAVTLTGROSLVLEVAVKMKQDVSMRBMISDFCERK 199

QY 154 HFVGHVHYFTIMVDVSRMPLIEGLRSKVKIKPEKRMODISMRRKKTIGEHIVAH 213  
 DB 214 IOHEVDLFCMDVQVQDKRGVETLGEVSAOOLAMWKADPNDFYERKRESAAYIPFG 273  
 DB 260 EGDFFYHAIIGGPTPOVNLITQECFKGLDKKNDIEAOMHDSHLNKKYFLNKPITKL 333  
 DB 320 SPEYLMDOQLGMPAVLRLKRLFTAVPKHQAVERN 353

QY 334 SPEYCMWYH-IGLPADIKLVKMSQTKKEYNVARN 366  
 DB 240 SPEYLMDOQLGMPAVLRLKRLFTAVPKHQAVERN 273



Query Match 32.6%; Score 655; DB 4; Length 274;  
 Best Local Similarity 45.3%; Pred. No. 3.8e-46;  
 Matches 124; Conservative 49; Mismatches 99; Indels 2; Gaps 2;

DB 94 RPEVNTMTKKAAPVVEGTYNNKAVLDNYAKOKITVGLVFAVNGRTIEHYLEFLTSANK 153  
 1 KKVAVLVTPWLAIVWEGTFNIDITNEQFLDONTTIGLVFAIKKYVA-FLKLFLETAEK 59  
 DB 154 HFWGHPVIFYIMVDVDSMPLELGLPLKSFYFKIKPEKRWODISMMKMTIGEHIVAH 213  
 60 HFWGHPVIFYIMVDVDSMPLELGLPLKSFYFKIKPEKRWODISMMKMTIGEHIVAH 119  
 DB 214 IOHEVDFLECMDDVDFODKFGVETLIGESVAOLQAMWKADPNDFYERKESAAVIFPG 273  
 120 FLSEVDVLCVDDMEFRHVGVEITLPLFGTLHPGFGSSREAFYERRPOQAVIFPD 179  
 DB 274 EGDFYHAAIFGCTPTQVINTOECFGKILKDKNDIEQWHDHSHLNKYFLINKPTKIL 333  
 180 EGDFYHAAIFGCTPTQVINTOECFGKILKDKNDIEQWHDHSHLNKYFLINKPTKIL 239  
 DB 334 SPEYCMDYH-TGLPADIKLVKMSWOTKRYNVVN 366  
 240 SPEYMDQQLGMPAVLRKRLRFTAVPKKNHOAVRN 273  
 DB  
 RESULT 10  
 0901R1 PRELIMINARY: PRI: 274 AA.  
 AC 0901R1:  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
 DE ABO GLYCOSYLTRANSFERASE (FRAGMENT).  
 GN ABO.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCHI\_TaxID=9606;  
 RN NCHI\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RA YIP S.P.;  
 RT \*Single-tube multiplex PCR-SSCP analysis distinguishes seven common  
 RT ABO alleles and readily identifies new alleles.\*  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF182746; AAF07060.1;  
 DR EMBL: AF182745; AAF07060.1; JOINED.  
 DR InterPro: IPR002369;  
 DR ProDom: P0001811; ; 1;  
 KW Transferase.  
 FT NON\_TER 1  
 FT NON\_TER 274  
 SU SEQUENCE 274 AA; 32020 MW; 11774AC648954AB6 CRC64;

Query Match 32.6%; Score 655; DB 4; Length 274;  
 Best Local Similarity 45.3%; Pred. No. 3.8e-46;  
 Matches 124; Conservative 49; Mismatches 99; Indels 2; Gaps 2;

DB 94 RPEVNTMTKKAAPVVEGTYNNKAVLDNYAKOKITVGLVFAVNGRTIEHYLEFLTSANK 153  
 1 KKVAVLVTPWLAIVWEGTFNIDITNEQFLDONTTIGLVFAIKKYVA-FLKLFLETAEK 59  
 DB 154 HFWGHPVIFYIMVDVDSMPLELGLPLKSFYFKIKPEKRWODISMMKMTIGEHIVAH 213  
 60 HFWGHPVIFYIMVDVDSMPLELGLPLKSFYFKIKPEKRWODISMMKMTIGEHIVAH 119  
 DB 214 IOHEVDFLECMDDVDFODKFGVETLIGESVAOLQAMWKADPNDFYERKESAAVIFPG 273  
 120 FLSEVDVLCVDDMEFRHVGVEITLPLFGTLHPGFGSSREAFYERRPOQAVIFPD 179  
 DB 274 EGDFYHAAIFGCTPTQVINTOECFGKILKDKNDIEQWHDHSHLNKYFLINKPTKIL 333

DB 180 EGDFYHAAIFGCTPTQVINTOECFGKILKDKNDIEQWHDHSHLNKYFLINKPTKIL 239  
 DB 334 SPEYCMDYH-TGLPADIKLVKMSWOTKRYNVVN 366  
 240 SPEYMDQQLGMPAVLRKRLRFTAVPKKNHOAVRN 273  
 DB

RESULT 11  
 0901R1 PRELIMINARY: PRI: 348 AA.  
 AC 0901R1:  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
 DE N-ACETYLGLYCOSAMINYLTRANSFERASE A BLOOD GROUP-LIKE ENZYME.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCHI\_TaxID=10116;  
 RN NCHI\_TaxID=10116;  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-BDIX; TISSUE=STOMACH;  
 RA Valdey B., Marionneau S., Calileau-Thomas A.L., Bouhours D.,  
 RA Le Pendu J.;  
 RT \*Rat N-acetylgalactosaminyltransferase A blood group-like enzyme.\*  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF264018; AAF74758.2;  
 KW Transferase.  
 SU SEQUENCE 348 AA; 40375 MW; FC5E572B10ED7B3 CRC64;

Query Match 32.6%; Score 654; DB 1; Length 348;  
 Best Local Similarity 45.3%; Pred. No. 6.3e-46;  
 Matches 124; Conservative 48; Mismatches 100; Indels 2; Gaps 2;

DB 94 RPEVNTMTKKAAPVVEGTYNNKAVLDNYAKOKITVGLVFAVNGRTIEHYLEFLTSANK 153  
 76 RNDVAVLFTWMLPFIWEGTFNIDITNEQFLDONTTIGLVFAIKKYVA-FLKLFLETAEK 134  
 DB 154 HFWGHPVIFYIMVDVDSMPLELGLPLKSFYFKIKPEKRWODISMMKMTIGEHIVAH 213  
 135 HFWGHPVIFYIMVDVDSMPLELGLPLKSFYFKIKPEKRWODISMMKMTIGEHIVAH 194  
 DB 214 IOHEVDFLECMDDVDFODKFGVETLIGESVAOLQAMWKADPNDFYERKESAAVIFPG 273  
 195 IOHEVDFLECMDDVDFODKFGVETLIGESVAOLQAMWKADPNDFYERKESAAVIFPG 254  
 DB 274 EGDFYHAAIFGCTPTQVINTOECFGKILKDKNDIEQWHDHSHLNKYFLINKPTKIL 333  
 255 EGDFYHAAIFGCTPTQVINTOECFGKILKDKNDIEQWHDHSHLNKYFLINKPTKIL 314  
 DB 334 SPEYCMDYH-TGLPADIKLVKMSWOTKRYNVVN 366  
 315 SPEYMDQQLGMPAVLRKRLRFTAVPKKNHOAVRN 348  
 DB

RESULT 12  
 0901R1 PRELIMINARY: PRI: 274 AA.  
 AC 0901R1:  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)  
 DE ABO GLYCOSYLTRANSFERASE (FRAGMENT).  
 GN ABO.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OC NCHI\_TaxID=9544;  
 RN NCHI\_TaxID=9544;  
 RP SEQUENCE FROM N.A.



DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)  
 DE 0-SPECIFIC ALPHA 1->3 N-ACETYLGLACTOSAMINYLTTRANSFERASE (FRAGMENT).  
 GN ABO.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yamamoto F.;  
 RI \*Human histo-blood group ABO gene locus alleles\*;  
 RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF134440; AAD26584.1;  
 DR EMBL: AF134439; AAD26584.1; JOINED.  
 KW Transferase.  
 FT NON\_TER 1 1  
 FT NON\_TER 274 274  
 SO SEQUENCE 274 AA: 31961 MD: 06D300E8022AF4B6 CRC64:

Query Match 32.4%; Score 650; DB 4; Length 274;  
 Best Local Similarity 45.3%; Pred. No. 9, 8e-46;  
 Matches 124; Conservative 48; Mismatches 100; Indels 2; Gaps 2;  
 QY 94 RPEVVTMTKKALVVEGTYNRAVLDNYAKOKITGLTFVAGRYIEHYLEPITSANK 153  
 Db 1 RKDVLVTFMLADIVWEGTFNIDILNQGFRIDNTITGLTFVFAIKRYA-FLKLFLETAEK 59  
 QY 154 HFWVGHPRVIFYIVNDVDSRMLIELGLPLSKFYFKIKPEKRWODISMRKKTIGENIHVAH 213  
 Db 60 HFWVGHPRVIFYIVNDVDSRMLIELGLPLSKFYFKIKPEKRWODISMRKKTIGENIHVAH 119  
 QY 214 IQHEVDPLFCMDVDVQDFQDKFVEYELGESVYAOIQAMWYKADPNDFYERKRESAYIPFG 273  
 Db 120 FLSEVDYLVCVDVDMERHGVVEILPLPLGTLHPFGSSREAFYERRPOSQATIPKD 179  
 QY 274 EGDFTYHAALFGSTPTQVLNITQECFKGLDKKNDIEAQWHDESHLNKYFLINKPTKIL 333  
 Db 180 EGDFTYLGRTFGSSVQEVQELTRACHQAMVVDQANGIEAWHDESHLNKYLLRHKPTKYL 239  
 QY 334 SPEYCMQDYH-IGLPADIKLVKMSWQTKENVVEN 366  
 Db 240 SPEYLMQDQILLGMPAVLRKIRPTAVPRKHQAVRN 273

Search completed: November 5, 2001, 15:22:21  
 Job time: 8384 sec

1  
2  
3